## AMENDMENTS TO THE SPECIFICATION

*Please replace the paragraph on page 45, lines 3-21, with the following:*

Capture oligonucleotides of various lengths, including 20, 21, 24, or 26 nucleotides (FV-WT20 (SEQ ID NO: 13): 5'(GGACAGGCGAGGAATACAGG)-(PEG)x3-$NH_2$, 3' FV-mut21 (SEQ ID NO: 14): 5'(TGGACAGGCAAGGAATACAGG)-(PEG)x3-$NH_2$ 3', FV-wt24 (SEQ ID NO: ~~153~~): 5' TGG ACA GGC GAG GAA TAC AGG TAT-$NH_2$ 3', FV-mut26 (SEQ ID NO: ~~164~~): 5' CTG GAC AGG CAA GGA ATA CAG GTA TT-$NH_2$ 3') were printed on CodeLink slides as described above and were added to 5 μg of normal human placenta genomic DNA (Sigma, St. Louis, MO) or factor V mutant human genomic DNA (isolated from repository culture GM14899, factor V deficiency, Coriell Institute). The slides and DNA were incubated in 20% FM, 30% FM, or 40% FM, and 4X SSC/0/04% Tween at 40°C for 2 hours in the first step. The slides were then washed in 2XSSC at room temperature for 3 minutes. After washing, nanoparticle probes with detection oligonucleotides that recognized Factor V were added and the mixture was then incubated for 1 hour at 40°C. The signal was detected by silver staining as described above. The results showed that under optimally tuned conditions (30% FM in this case), the human wt DNA generated a signal on the wt probes only, while the human mutant DNA generated a signal only at the mutant capture probes (Figure 8). Changing the stringency conditions resulted in either loss of discrimination (stringency too low) or loss of signal (stringency too high). Figure 9 shows the quantitative data for the perfect (center) hybridization condition in Figure 8.

*Please replace the table, on page 49 of the specification and labeled as Table 1, with the following:*

| | | TM calculated with HyTher™ (Wayne State University) | | |
|---|---|---|---|---|
| | | No corrections | TM correction for hybridization to surface bound probes according to: | |
| | | (35%FM) | Santalucia et al. (35%FM) | Fotin et al. (35%FM) |
| **Capture** | **Sequence** | | | |
| FII-SNP/Cap1-wt22 (SEQ ID NO: 5) | CTCAGCGAGCCTCAATGCTCCC | 46.7 | **37.0** | 45.0 |
| FII-SNP/Cap1-mut23 (SEQ ID NO: 6) | **CTCTCAGCAAGCCTCAATGCTCC** | 47.2 | **35.7** | 46.3 |
| MTHFR-SNP/Cap6-wt22 (SEQ ID NO: 61) | **GATGAAATCGGCTCCCGCAGAC** | 40.3 | **35.5** | **43.0** |
| MTHFR-SNP/Cap7-mut22 (SEQ ID NO: 2) | **ATGAAATCGACTCCCGCAGACA** | 40.7 | **36.2** | **44.0** |
| FV-Cap-WT-24 (SEQ ID NO: ~~153~~) | TGGACAGGCGAGGAATACAGGTAT | 44.8 | **35.5** | 42.9 |
| FV-Cap-mut26 (SEQ ID NO: ~~164~~) | CTGGACAGGCAAGGAATACAGGTATT | 44.5 | **35.8** | 42.9 |
| **Probe** | | | | |
| FV-46 (SEQ ID NO: ~~129~~) | 5' Epi- CCA CAG AAA ATG ATG CCC AGT GCT TAA CAA GAC CAT ACT ACA GTG A 3' | 54.8 | 49.2 | 57.6 |
| FII-ProI-47 (SEQ ID NO: ~~107~~) | 5' Epi-TCC TGG AAC CAA TCC CGT GAA AGA ATT ATT TTT GTG TTT CTA AAA CT 3' | 52.2 | 46.9 | 54.8 |
| MTHFR-Pro II-58 (SEQ ID NO: 8) | 5' Epi-AAA GAT CCC GGG GAC GAT GGG GCA AGT GAT GCC CAT GTC GGT GCA TGC CTT CAC AAA G 3' | 68.4 | 58.6 | 68.5 |